



Atty. Docket No.: 25436/1190

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Sorge
Serial No.: 09/709,945
Filed: November 10, 2000
Entitled: Gene Monitoring and Gene
Identification Using cDNA
Arrays

Examiner: B. Sisson

Group Art Unit: 1634

Conf. No.: 3915

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8a

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Commissioner for Patents
Washington, D.C. 20231

TECH CENTER 1600/2900

AMENDMENT AND RESPONSE TO OFFICE ACTION

This Amendment is filed in response to the Office Communication, dated February 6, 2002, in the above-identified application.

IN THE SPECIFICATION:

On page 22, please replace the first paragraph with the following:

Search tools such as the Basic Local Alignment Search Tool ("BLAST") can also be used to identify cDNAs having substantial sequence identity to one or more sequences in a public database. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (located on the world wide web at ncbi.nlm.nih.gov/). The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, Proc. Nat'l. Acad. Sci. USA 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered substantially identical to a reference sequence if the smallest sum probability in a comparison of the cDNA to the reference nucleic acid is less than about 0.001.